FIG. 1A

```
      GTCCTTCCACCATGCACTCGCTGGCTTCTTCTGTGGGTGTTCTCTGCTCGCCGCTG
   1  -----+----+----+----+----+----+----+----+----+----+---- 60
      CAGGAAGGTGGTACGTGAGCGACCGAAGAAGAGACACCGCAAGAGAGCGAGCGGCGAC
          M  H  S  L  G  F  F  S  V  A  C  S  L  L  A  A  -

      CGCTGCTCCGGGTCCTCGAGGGCCCGCGCCGGCCTTCGAGTCCGGACTCG
  61  -----+----+----+----+----+----+----+----+----+----+---- 120
      GCGACGAGGCCCAGGAGCGCTCCGGGCGCGGCGGCGAAGCTCAGGCCTGAGC
          L  L  P  G  P  R  E  A  P  A  A  A  A  F  E  S  G  L  D  -

      ACCTCTCGGACGCGGGAGCCCGACGCGGCGAGCCACGGCTTATGCAAGCAAAGATCTGG
 121  -----+----+----+----+----+----+----+----+----+----+---- 180
      TGGAGAGCCTGCGCCCTCGGGCTGCGCCCGGTGCCGAATACGTTCGTTCTAGACC
          L  S  D  A  E  P  D  A  G  E  A  T  A  Y  A  S  K  D  L  E  -

      AGGAGCAGTTACGGTCTGTGTCCAGTGTGAGAACTCATGACTGTACTCTCACCCAGAAT
 181  -----+----+----+----+----+----+----+----+----+----+---- 240
      TCCTCGTCAATGCCAGACACAGTCACATCTTACTGAGTACTGACATGAGATGGGTCTTA
          E  Q  L  R  S  V  S  S  V  D  E  L  M  T  V  L  Y  P  E  Y  -

      ATTGGAAAATGTACAAGTGTCAGTTACAAGGAAAGGAGGCTGCAACATAACAGAGAACAGG
 241  -----+----+----+----+----+----+----+----+----+----+---- 300
      TAACCTTTACATGTTCACAGTCGATTCCTTTCCTCCGACCGTTGTATTGTCTCTTGTCC
          W  K  M  Y  K  C  Q  L  R  K  G  G  W  Q  H  N  R  E  Q  A  -

      CCAACCTCAACTCAAGGACAGAAGAGACTATAAAATTGCTGCAGCACATTATAATACAG
```

MATCH WITH FIG. 1B

FIG. 1B

MATCH WITH FIG. 1A

```
301  GGTTGGAGTTGAGTTCCTGTCTTCTTCTGATATTTAAACGACGTCGTGTAATATTATGTC  360
     ----+---------+---------+---------+---------+---------+
     AGATCTTGAAAAGTATTGATAATGAGTGGAGAAAGACTCAATGCCATGCCACGGGAGGTGT
C     N  L  N  S  R  T  E  E  T  I  K  F  A  A  H  Y  N  T  E  -

361  TCTAGAACTTTCATAACTATTACTCACCTCTTCTGAGTTACGGTGCCCTCCACA        420
     ----+---------+---------+---------+---------+---------+
     AGATCTTGAAAAGTATTGATAATGAGTGGAGAAAGACTCAATGCCATGCCACGGGAGGTGT
C     I  L  K  S  I  D  N  E  W  R  K  T  Q  C  M  P  R  E  V  C  -

421  CATATCTACACCCCTTCCTCAAACCTCAGCGCGTGTTGTGAAGAAATTGGAGTACAC     480
     ----+---------+---------+---------+---------+---------+
     GTATAGATGTGGGGGAAGGAGTTGGAGT
C     I  D  V  G  K  E  F  G  V  A  T  N  T  F  F  K  P  P  C  V  -

481  ACAGGCAGATGTCTACACCCCCAACGACGTTATCACTCCCCACGTACTGTGGT        540
     ----+---------+---------+---------+---------+---------+
     TGTCCGTCTACAGAGATGTGGGGGTTGCTGCAATAGTGAGGGGCTGCAGTGCATGAACACCA
C     S  V  Y  R  C  G  G  C  N  S  E  G  L  Q  C  M  N  T  S  -

541  CGTGCTCGATGGAGTCGTTCTGCAATAAACTTTAATGTCACGGAGAGAGTTCCGGGGT    600
     ----+---------+---------+---------+---------+---------+
     GCACGAGCTACCTCAGCAAGACGTTATTTGAAATTACAGTGCCCTCTCTCTCCAAGGCCCCA
C     T  S  Y  L  S  K  T  L  F  E  I  T  V  P  L  S  Q  G  P  K  -

601  TTGGTCATTGTTAGTCAAAACGGTTAGTGTGAAGGACGGCTACGTACAGATTGACCTAC   660
     ----+---------+---------+---------+---------+---------+
     AACCAGTAACAATCAGTTTGCCAATCACACTTCCTGCCGATGCATGTCTAAACTGGATG
C     P  V  T  I  S  F  A  N  H  T  S  C  R  C  M  S  K  L  D  V  -
```

MATCH WITH FIG. 1C

FIG. 1C

MATCH WITH FIG. 1B

```
661  TTACAGACAAGTTCATTCCATTATTAGACGTTCCCTGCCAGCAACACTACCACAGTGTC
     ---------+---------+---------+---------+---------+---------+ 720
     AAATGTCTGTTCAAGTAAGGTAATAATCTGCAAGGACGGTCGTTGTGATGGTGTCACAG
              Y  R  Q  V  H  S  I  R  R  S  L  P  A  T  L  P  Q  C  Q  -
C

721  AGGCAGGCGAACAAGACCTGCCCCACCAATTACACATGTGGAATAATCACATCTGCAGATGCC
     ---------+---------+---------+---------+---------+---------+ 780
     TCCGTCGCTTGTTCTGGACGGGGTGGTTAATGTGTACACCTTATTAGTGTAGACGTCTACGG
              A  A  N  K  T  C  P  T  N  Y  M  W  N  N  H  I  C  R  C  L  -
C

781  TGGCTCAGGAAGATTTATGTTTCCTCGGATGCTGGAGATGACTCAACAGATGGATTCC
     ---------+---------+---------+---------+---------+---------+ 840
     ACCGAGTCCTTCTAAATACAAAAGGAGCCTACGACCTCTACTGAGTTGTCTACCTAAGG
              A  Q  E  D  F  M  F  S  S  D  A  G  D  D  S  T  D  G  F  H  -
C

841  ATGACATCTGTGGACCAAACAAGGAGCTGGATGAAGAGACCTGTCAGTGTGTCTGCAGAG
     ---------+---------+---------+---------+---------+---------+ 900
     TACTGTAGACACCTGGTTTGTTCCTCGACCTACTTCTCTGGACAGTCACACAGACGTCTC
              D  I  C  G  P  N  K  E  L  D  E  E  T  C  Q  C  V  C  R  A  -
C

901  CGGGGCTTCGGCCTGCCAGCTGTGGACCCCACAAAGAACTAGACAGAAACTCATGCCAGT
     ---------+---------+---------+---------+---------+---------+ 960
     GCCCCGAAGCCGGACGGTCGACACCTGGGGTGTTCTTGATCTGTCTTTGAGTACGGTCA
              G  L  R  P  A  S  C  G  P  H  K  E  L  D  R  N  S  C  Q  C  -
C

961  GTGTCTGTAAAAACAAACTCTTCCCCAGCCAATGTGGGGCCAACCGAGAATTGATGAAA
     ---------+---------+---------+---------+---------+---------+ 1020
     CACAGACATTTTGTTTGAGAAGGGGTCGGTTACACCCCGGTTGGCTCTTAAACTACTTT
```

MATCH WITH FIG. 1D

FIG. 1D

```
              V  C  N  K  L  F  P  S  Q  C  G  A  N  R  E  F  D  E  N  -

      ACACATGCCAGTGTGTATGTAAAAGAACCTGCCCAGAAATCAACCCTAAATCCTGGAA
1021  -------+---------+---------+---------+---------+---------+ 1080
      TGTGTACGGTCACACATACATTTCTTGGACGGGTCTTTAGTTGGGGATTTAGGACCTT
              T  C  Q  C  V  C  K  R  T  C  P  R  N  Q  P  L  N  P  G  K  -

      AATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTAAAAGGAAAGAAGTTCC
1081  -------+---------+---------+---------+---------+---------+ 1140
      TTACACGGACACTTACATGTCTTTCAGGTGTCTTTACGAACAATTTCCTTCTTCAAGG
              C  A  C  E  C  T  E  S  P  Q  K  C  L  L  K  G  K  K  F  H  -

      ACCACCAAACATGCAGCTGTTACAGACGGCCATGTACAGCGGCCAGAAGGCTTGTGAGC
1141  -------+---------+---------+---------+---------+---------+ 1200
      TGGTGGTTTGTACGTCGACAATGTCTGCCGGTACATGTCGCCGGTCTTCCGAACACTCG
              H  Q  T  C  S  C  Y  R  R  P  C  T  N  R  Q  K  A  C  E  P  -

      CAGGATTTTCATATAGTGAAGAAGTGTGTCGTTGTGTCCCTTCATATTGGCAAAGACCAC
1201  -------+---------+---------+---------+---------+---------+ 1260
      GTCCTAAAGTATATCACTTCTTCACACAGCAACACAGGAAGTATAACCGTTTCTGGTG
              G  F  S  Y  S  E  E  V  C  R  C  V  P  S  Y  W  Q  R  P  Q  -

      AAATGAGCTAAGATTGTACTGTTTCCAGTTCATCGATTTCTATTATGGAAAACTGTGT
```

FIG. 1E

MATCH WITH FIG. 1D

```
1261 ------+---------+---------+---------+---------+---------+ 1320
     TTACTCGATTCTAACATGACAAAGGTCAAGTAGCTAAAAGATAATACCTTTGACACA
              M  S  *
   C

1321 ------+---------+---------+---------+---------+---------+ 1380
     TGCCACAGTAGAACTGTCTGTGAACAGAGAGACCCTTGTGGGTCCATGCTAACAAAGACA
     ACGGTGTCATCTTGACAGACACTTGTCTCTCGGGAACACCCAGGTACGATTGTTTCTGT

1381 ------+---------+---------+---------+---------+---------+ 1440
     AAAGTCTGTCTTTCCTGAACCATGTGGATAACTTACAGAAAATGGACTGGAGCTCATCTG
     TTTCAGACAGAAAGGACTTGGTACACCTATTGAAATGTCTTTACCTGACCTCGAGTAGAC

1441 ------+---------+---------+---------+---------+---------+ 1500
     CAAAAGGCCCTCTGTAAAGACTGGTTTCTGCCAATGACCAAACAGCCAAGATTTCCTC
     GTTTTCCGGAGAACATTCTGACCAAAGACGGTTACTGGTTTGTGCGGTTCTAAAAGGAG

1501 ------+---------+---------+---------+---------+---------+ 1560
     TTGTGATTCTTTAAAAGAATGACTATATATAATTTATTCCACTAAAAATATTGTTTCTGC
     AACACTAAAGAAATTTCTTACTGATATATTAAATAAAGGTGATTTTATAACAAAGACG

1561 ------+---------+---------+---------+---------+---------+ 1620
     ATTCATTTTATAGCAACAACAATTGGTAAAACTCACTGTGATCAATATTTTATATCAT
     TAAGTAAAAATATCGTTGTTGTTAACCATTTGAGTGACACTAGTTATAAAAATATAGTA

1621 ------+---------+---------+---------+----- 1674
     GCAAAATATGTTAAAATAAAAATGAAAATTGTATTTATAAAAAAAAAAAAAAA
     CGTTTTATACAATTTTATTTACTTTAACATAAATATTTTTTTTTTTTT
```

1   CGAGGCCACGGCTTATGCAAGCAAAGATCTGGAGGAGCAGTTACGGTCTCTGTGTCCAGTGT
    ----+----+----+----+----+----+

71 AGATGAACTCATGACTGTACTCTACCCAGAATATATTGGAAAATGTACAAGTGTCAGCTAAG
    ----+----+----+----+----+----+
         M T V L Y P E Y W K M Y K Q L R

121 GAAAGGAGGCTGGCAACATAACAGAGAACAGGCCAACCTCAACTCAAGGACAGAAGAGAC
    ----+----+----+----+----+----+
    K G G W Q H N R E Q A N L N S R T E E T

181 TATAAAATTTGCTGCAGCACACATTATATAACAGAGATCTGAAAAGTATTGATAATGAGTG
    ----+----+----+----+----+----+
    I K F A A A H Y N T E I L K S I D N E W

241 GAGAAAGACTCAATGCATGCCACGGGGAGGTGTGTATAGATGTGGGGAAGGAGTTTGGAGT
    ----+----+----+----+----+----+
    R K T Q C M P R E V C I D V G K E F G V

301 CGCGGACAAACACCTTCTTTAAACCTCCATGTGTCCGTCTACAGATGTGGGGGTTGCTG
    ----+----+----+----+----+----+
    A T N T F F K P P C V S V Y R C G G C C

FIG. 2A

361 CAATAGTGAGGGCTGCAGTGCATGAACACCAGCACGGAGCTACCTCAGCAAGACGTTATT
    ---------+---------+---------+---------+---------+---------+
     N S E G L Q C M N T S T S Y L S K T L F

421 TGAAATTACAGTGCCTCTCTCTCAAGGCCCCAAACCAGTAACAATCAGTTTGCCAATCA
    ---------+---------+---------+---------+---------+---------+
     E I T V P L S Q G P K P V T I S F A N H

481 CACTTCCTGCCGATGCATGTCTAAACTGGATGTTTACAGACAAGTTCATTCCATTATTAG
    ---------+---------+---------+---------+---------+---------+
     T S C R C M S K L D V Y R Q V H S I I R

541 ACGTTCCCTGCCAGCAACACTACCACAGTGTCAGGCAGGCGAACAAGACCTGCCCCACCAA
    ---------+---------+---------+---------+---------+---------+
     R S L P A T L P Q C Q A A N K T C P T N

601 TTACATGTGGAATAATCACATCTGCAGATGCCTGGCTCAGGAAGATTTTATGTTTCCTC
    ---------+---------+---------+---------+---------+---------+
     Y M W N N H I C R C L A Q E D F M F S S

661 GGATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTGTGGACCAAACAAGGAGCT
    ---------+---------+---------+---------+---------+---------+
     D A G D D S T D G F H D I C G P N K E L

FIG.2B

```
 721  GGATGAAGAGACCTGTCAGTGTGTCTGCGCAGAGCGGGGGCTTCGGCCTGCCAGCTGGACC
      ---------+---------+---------+---------+---------+---------+
       D  E  E  T  C  Q  C  V  C  R  A  G  L  R  P  A  S  C  G  P

 781  CCACAAGAACTAGACAGAAACTCATGCCAGTGTCTGTAAAACAAACTCTTCCCAG
      ---------+---------+---------+---------+---------+---------+
       H  K  E  L  D  R  N  S  C  Q  C  V  C  K  N  K  L  F  P  S

 841  CCAATGTGGGCCAACCGAGAATTTGATGAAAACACATGCCAGTGTGTATGTAAAAGAAC
      ---------+---------+---------+---------+---------+---------+
       Q  C  G  A  N  R  E  F  D  E  N  T  C  Q  C  V  C  K  R  T

 901  CTGCCCCAGAAATCAACCCCTAAATCCTGGAAAATGTGCCTGTGAATGTACAGAAAGTCC
      ---------+---------+---------+---------+---------+---------+
       C  P  R  N  Q  P  L  N  P  G  K  C  A  C  E  C  T  E  S  P

 961  ACAGAAATGCTTGTTAAAAGGAAAGAAGTTCCACCACCAAACATGCAGCTGTTACAGACG
      ---------+---------+---------+---------+---------+---------+
       Q  K  C  L  L  K  G  K  K  F  H  H  Q  T  C  S  C  Y  R  R

1021  GCCATGTACGAACCGCCAGAAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGAAGTGTG
      ---------+---------+---------+---------+---------+---------+
       P  C  T  N  R  Q  K  A  C  E  P  G  F  S  Y  S  E  E  V  C
```

FIG.2C

```
1081  TCGTTGTGTCCCTTCATATTGGCAAAGACCACAAATGAGCTAAGATTGTACTGTTTCCA
      ----+---------+---------+---------+---------+---------+
             R  C  V  P  S  Y  W  Q  R  P  Q  M  S

1141  GTTCATCGATTTCTATTATGGAAAACTGTGTTGCCACAGTAGAACGTCTGTGAACAGA
      ----+---------+---------+---------+---------+---------+

1201  GAGACCCTTGTGGGTCCATGCTAACAAGACAAAGTCTGTCTTTCCTGAACCATGTGGA
      ----+---------+---------+---------+---------+---------+

1261  TAACTTTACAGAAATGGACTGGAGCTCATCTGCAAAGGCCTCTTGTAAAGACTGGTTT
      ----+---------+---------+---------+---------+---------+

1321  CTGCCAATGACCAAACAGCCAAGATTTCCTCTTGTGATTTCTTTAAAGAATGACTATA
      ----+---------+---------+---------+---------+---------+

1381  TAATTTATTCCACTAAAAATATTGTTCTGCATTCATTTTTATAGCAACAACAATTGGT
      ----+---------+---------+---------+---------+---------+

1441  AAAACTCACTGTGATCAATATTTTATATCATGCAAAATATGTTTAAAATAAATGAAAA
      ----+---------+---------+---------+---------+---------+

1501  TTGTATTATAAAAAAAAAAAAAAA
      ----+---------+---
```

FIG.2D

```
                                                              50
Pdgfa   .MRTLACLLL  LGCGYLAHVL  AEEAEIPREV  IERLARSQIH  SIRDLQRLLE
Pdgfb   MNRCWA.LFL  SLCCYLRLVS  AEGDPIPEEL  YEMLSDHSIR  SFDDLQRLLH
Vegf    .....MNFLL  SWVHWSLALL  LY........  ..........  .LEHAKWSQA
Vegf2   .......MTV  LYPEYWKMYK  CQ........  ..........  .LRKGGWQHN

  51                                                         100
Pdgfa   IDSVGSEDSL  DTSLRAHGVH  ATKHVPEKRP  LPIRRKRSI.  .....EEAVP
Pdgfb   GDP.GEEDGA  ELDLNMTRSH  SGGELES...  .LARGRRSLG  SLTIAEPAMI
Vegf    APMAE.....  ......GGGQ  NHHEVVKFMD  .VYQR.....  ..........
Vegf2   REQANLNSRT  EETIKFAAAH  YNTEILKSID  NEWRK.....  ..........

 101                                                         150
Pdgfa   AVCKTRTVIY  EIPRSQVDPT  SANFLIWPPC  VEVKRCTGCC  NTSSVKCQPS
Pdgfb   AECKTRTEVF  EISRRLIDRT  NANFLVWPPC  VEVQRCSGCC  NNRNVQCRPT
Vegf    SYCHPIETLV  DIFQEYPDEI  ..EYIFKPSC  VPLMRCGGCC  NDEGLECVPT
Vegf2   TQCMPREVCI  DVGKEFGVAT  ..NTFFKPPC  VSVYRCGGCC  NSEGLQCMNT

 151                                                         200
Pdgfa   RVHHRSVKVA  KVEYVRKKPK  LKEVQVRLEE  HLECAC....  AT........
Pdgfb   QVQLRPVQVR  KIEIVRKKPI  FKKATVTLED  HLACKC....  ETVAAARPVT
Vegf    EESNITMQIM  RIK.PH..QG  QHIGEMSFLQ  HNKCECRPKK  DRARQEKKSV
Vegf2   STSYLSKTLF  EIT.VPLSQG  PKPVTISFAN  HTSCRCMSKL  DVYRQVHSII
```

FIG.3A

```
              201
Pdgfa         ...TSLNPD  YREEDTDVR.  ..........  ..........  ..........
Pdgfb         RSPGGSQEQR AKTPQTRVTI RTVRVRRPPK  GKHRKFKHTH  DKTALKETLG
Vegf          RGK.....:  .GKGQKRKRK KSRYKSWSVY  VGARCCLMPW  SLPGPHP...
Vegf2         RRSLPATLPQ CQAANKTCPT NYMWNNHICR  CLAQEDFMFS  SDAGDDSTDG
                                                           250

              251
Pdgfa         ..........  ..........  ..........
Pdgfb         A.........  ..........
Vegf          ...CGP....  ......CSE   RRKHLFVQDP  QTCKCSCKNT
Vegf2         FHDICGPNKE  LDEETCQCVC  RAGLRPASCG  PHKEL...DR  NSCQCVCKNK
                                                           300

              301
Pdgfa         ..........  ..........  ..........
Pdgfb         ..........  ..........
Vegf          .DSRCKARQ   LELNERTCRC  DKPRR.....  ......
Vegf2         LFPSQCGANR  .EFDENTCQC  VCKRTCPRNQ  PLNPGKCACE  CTESPQKCLL
                                                           350

              351
Pdgfa         ..........  ..........  ..........
Pdgfb         ..........  ..........
Vegf          ..........  ..........  ..........
Vegf2         KGKKFHHQTC  SCYRRPCTNR  QKACEPGFSY  SEEVCRCVPS  YWQRPQMS
                                                           398
```

FIG.3B

PERCENTAGE (%) OF AMINO ACID IDENTITIES BETWEEN EACH PAIR OF GENES IS SHOWN IN THE FOLLWING TABLE

	PDGFα	PDGFβ	VEGF	VEGF2
PDGFα				
PDGFβ	48.0			
VEGF	20.7	22.7		
VEGF2	23.5	22.4	30.0	

FIG.4

Expression of VEGF2 mRNA in Human Breast Tumor Cells
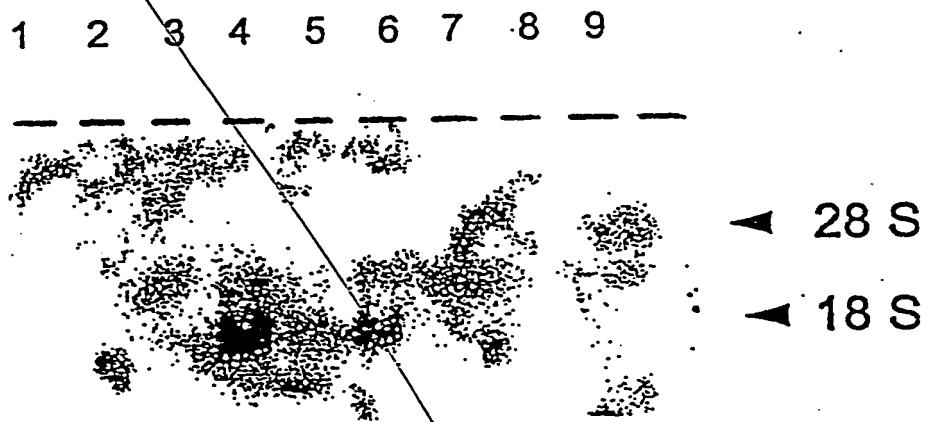
1. normal breast tissue
2. breast tumor tissue
3-9. breast tumor cell lines.

FIG. 5

9.5 kb
7.5 kb
4.4 kb
2.4 kb
1.4 kb

2.2 kb
1.3 kb

1   2   3   4   5   6   7   8   9   10

1. ovary	6. lung
2. testes	7. spleen
3. gall bladder	8. prostate
4. kidney	9. Hippocampus
5. liver	10. heart
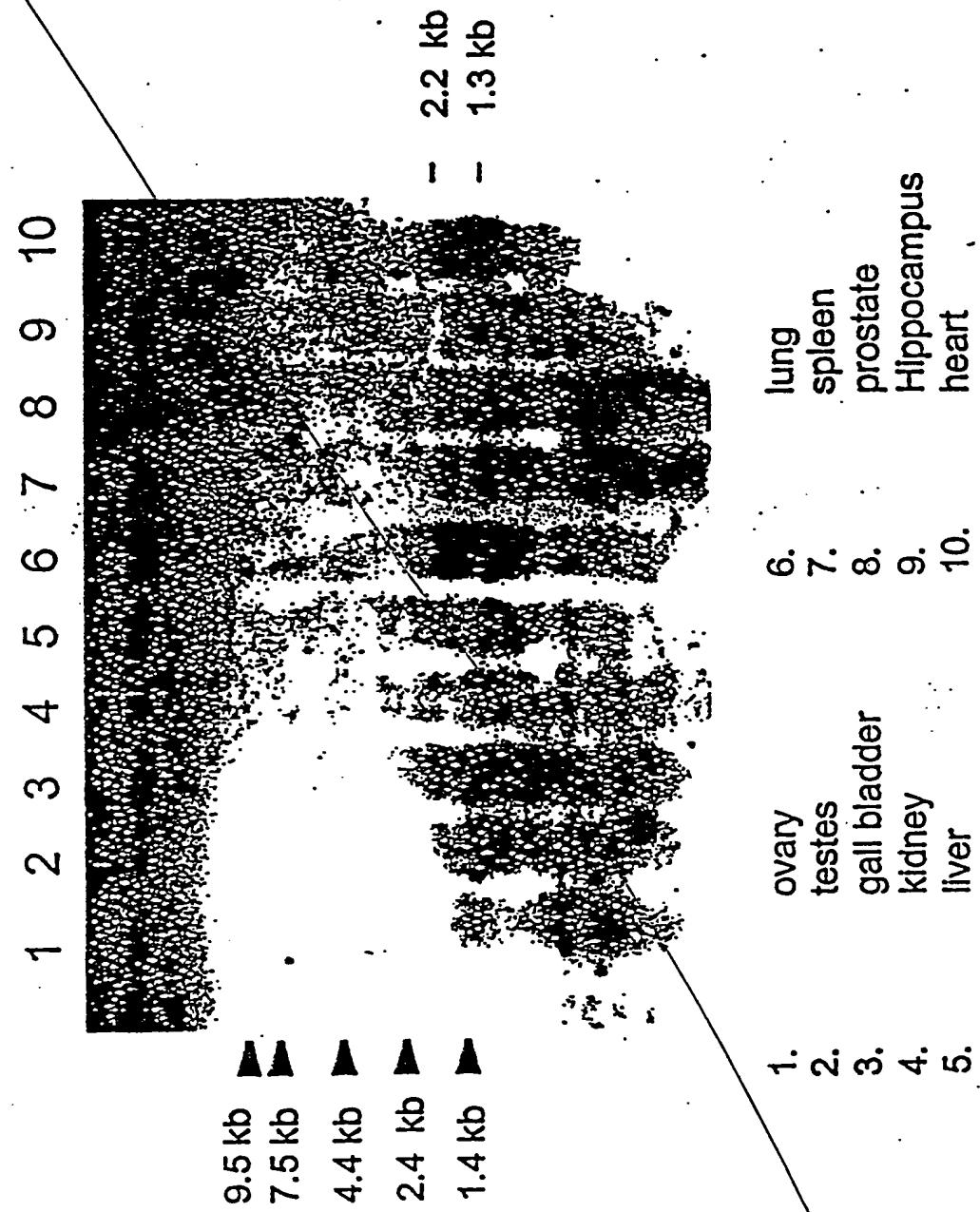
Expression of VEGF2 mRNA in human adult tissues.

FIG.6

F I G. 7

	1	2	3	4	5

200 kd ►

97 kd ►

69 kd ►

45 kd ►

— 39-40 kd
— 36-38 kd

30 kd ►

21 kd ►

14 kd ►

Lane 1: 14-C and rainbow M.W. marker
Lane 2: FGF control
Lane 3: VEGF2 (M13-reverse & forward primers)
Lane 4: VEGF2 (M13-reverse & VEGF-F4 primers)
Lane 5: VEGF2 (M13-reverse & VEGF-F5 primers)

reducing gel

M 1 M 2 M 3 4 M

210 —
98 —
67 —
45 —

30 —

21 —

14 —

Lane M: Marker
Lane 1: vector cytoplasm
Lane 2: vector medium
Lane 3: VEGF2 cytoplasm
Lane 4: VEGF2 medium

FIG. 8B

non-reducing gel

M 1 M 2 M

98 —

67 —

45 —

30 —

21 —

14 —

Lane M: Marker
Lane 1: vector medium
Lane 2: VEGF2 medium

FIG. 8A

FIG. 9

FIG. 10

98 kd –
68 kd –
43 kd –
29 kd –
18 kd –
14 kd –

1 2

M + β-ME   - β-ME

98 kd–
68 kd–
43 kd–
29 kd–
18 kd–
14 kd–

Lane 1:   Molelular weight marker
Lane 2.   Precipitates containing VEGF2.

FIG. II
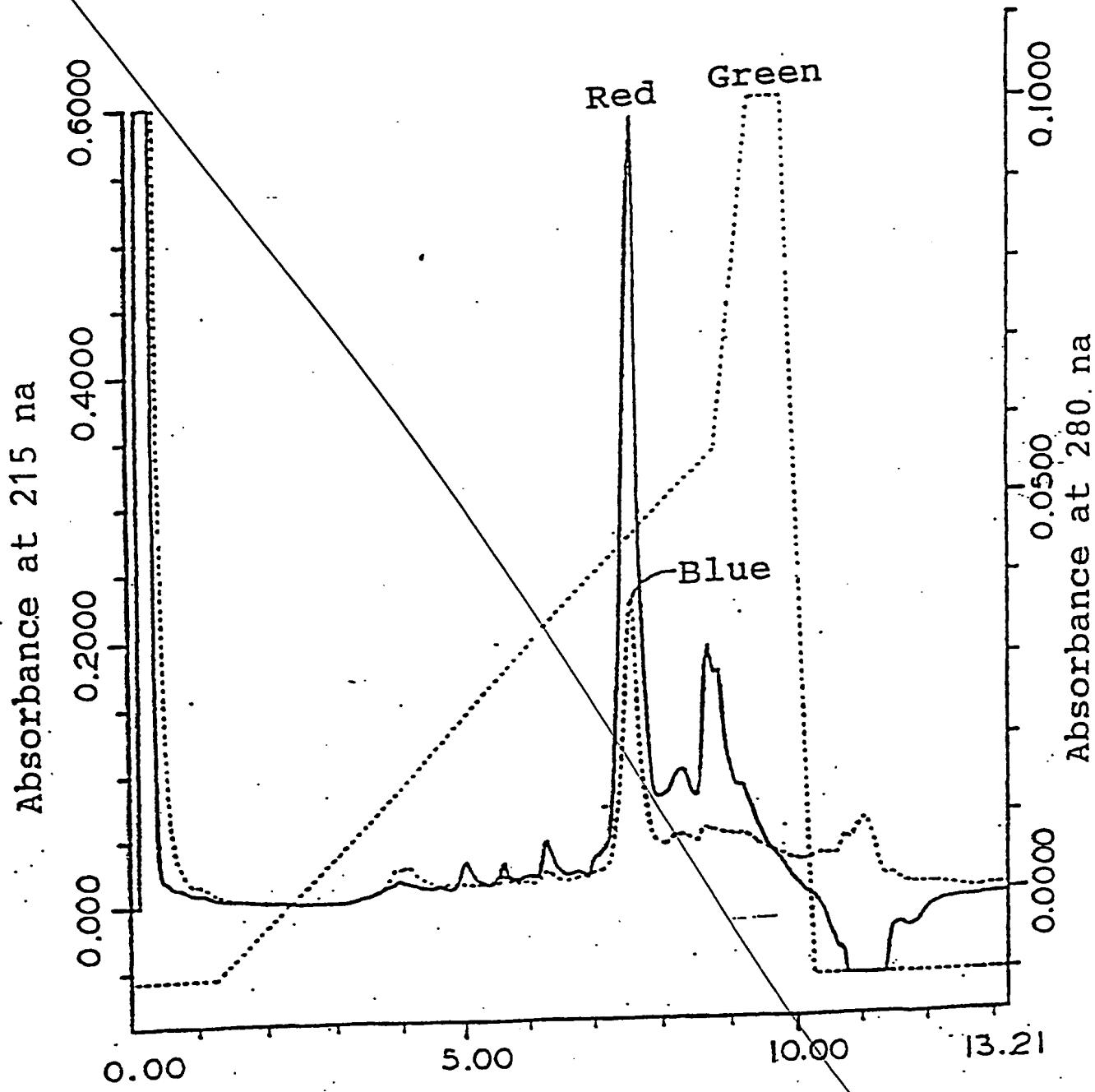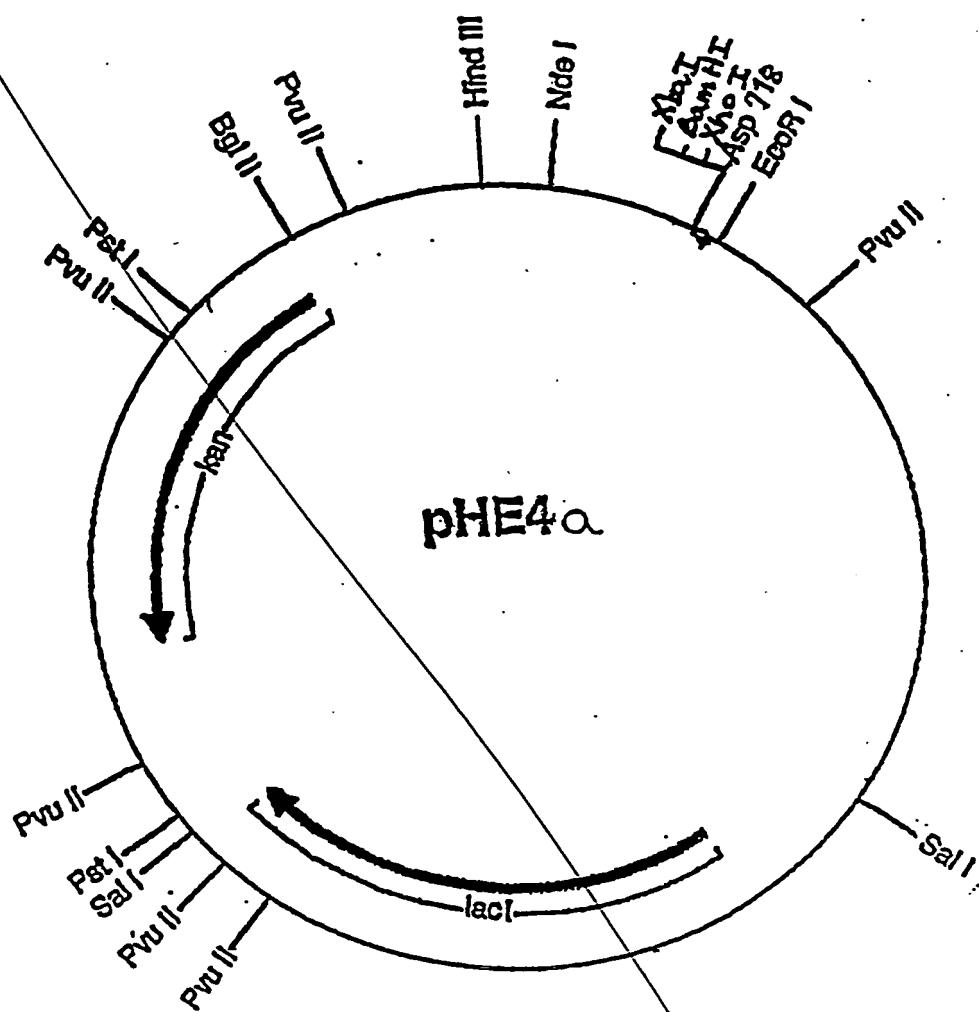
FIG. 12

FIG. 13
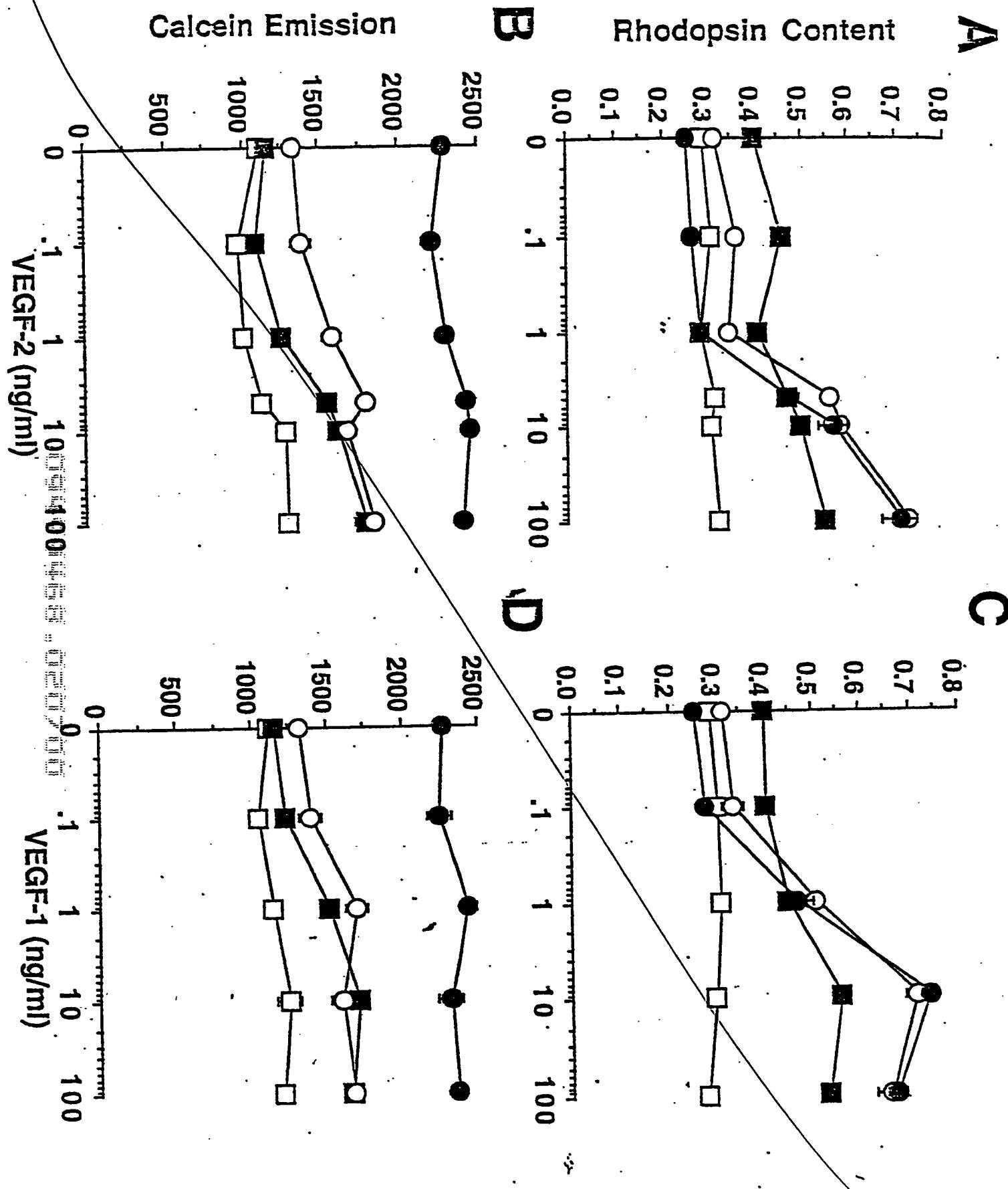
FIG. 14
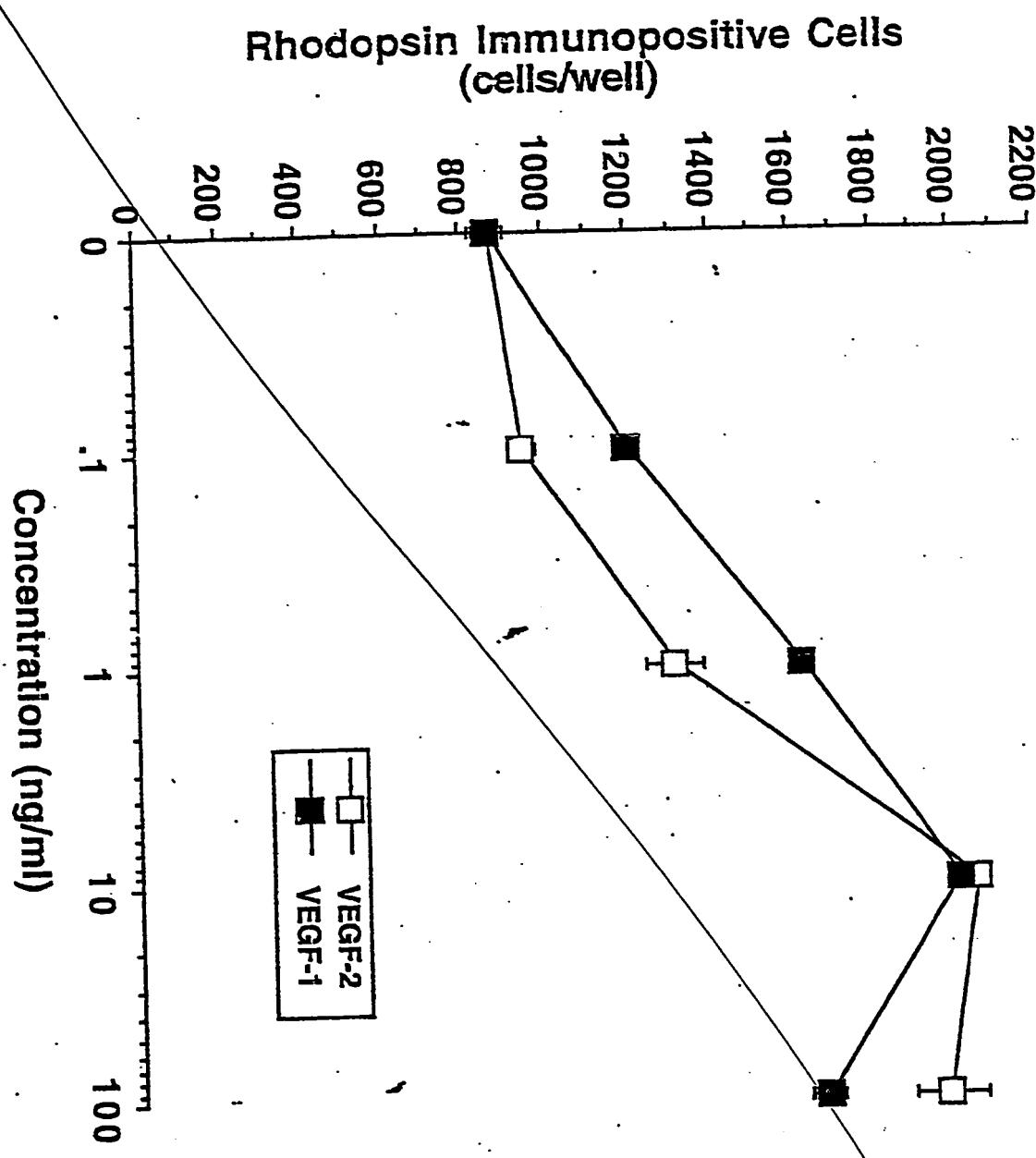
Rhodopsin Immunopositive Cells (cells/well)

Concentration (ng/ml)

VEGF-2
VEGF-1

FIG. 15

FIG. 16

FIG. 17

FIG.18

A

B

C

FIG. 19

VEGF-2 (ng/ml)

FIG. 20

FIG. 21.

A

Rhodopsin Content

Legend:
- □ CNTF
- ■ CNTF + VEGF-2

B

Calcein Emission

CNTF (ng/ml)

C
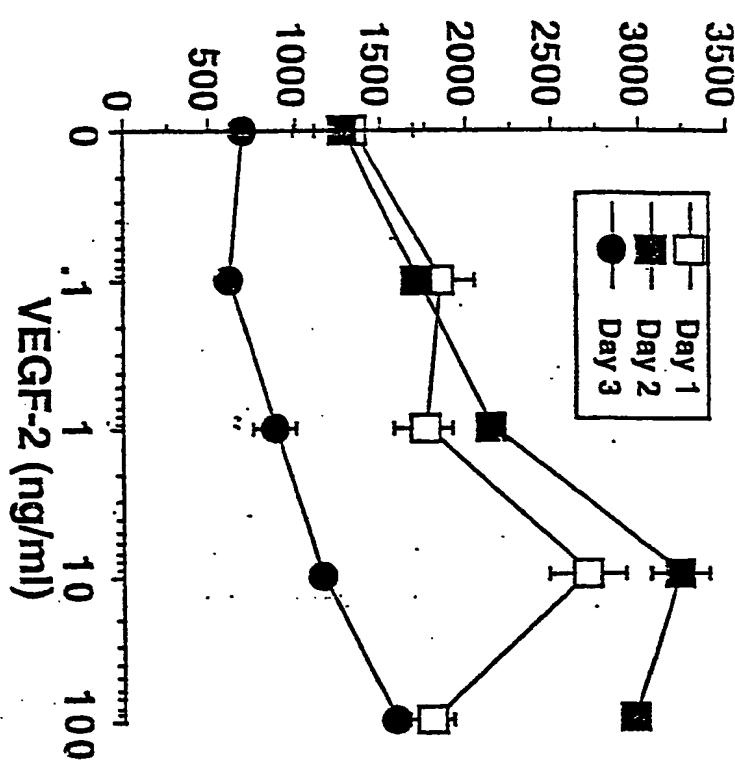
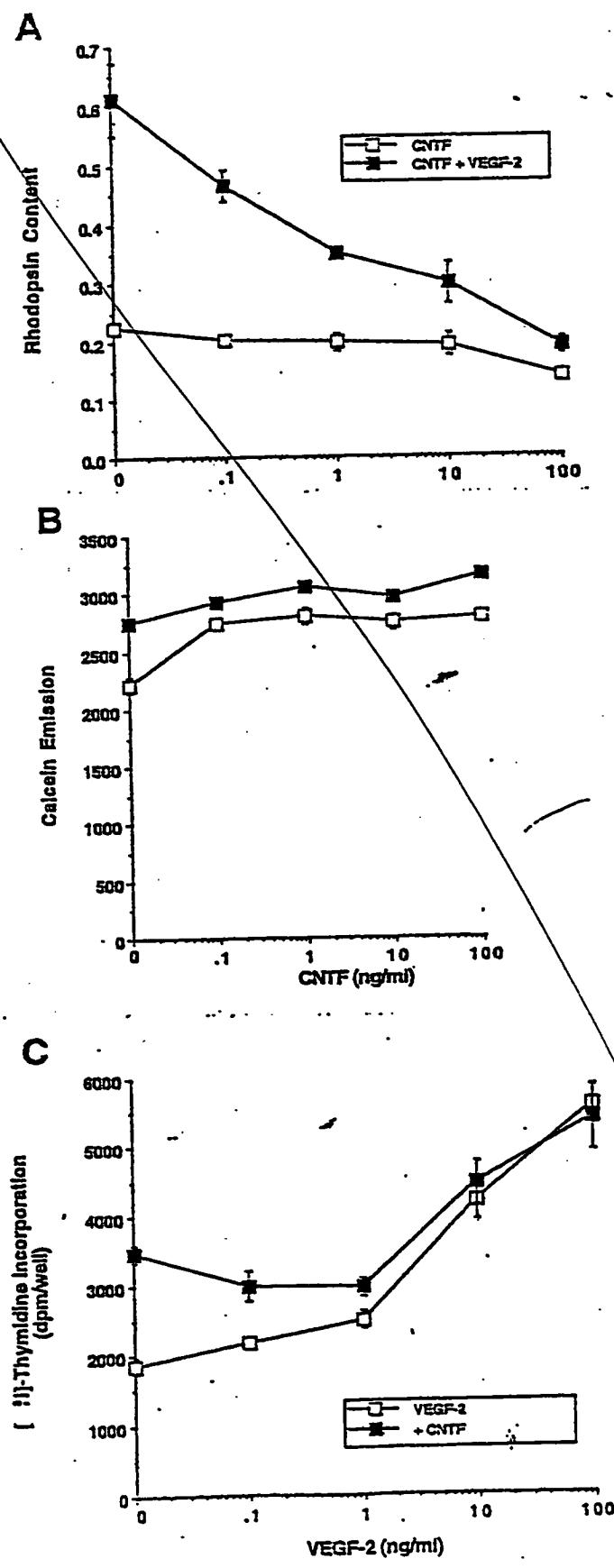[³H]-Thymidine Incorporation (dpm/well)

Legend:
- □ VEGF-2
- ■ + CNTF

VEGF-2 (ng/ml)
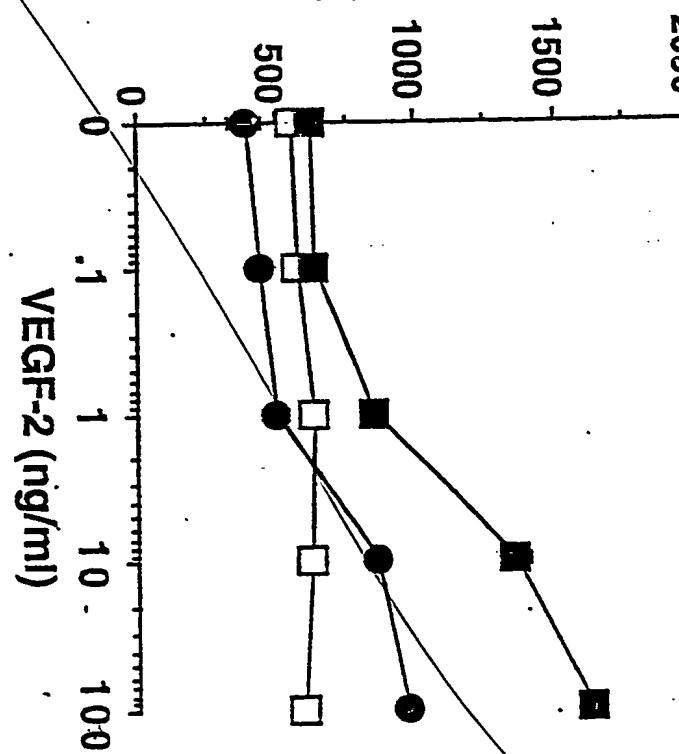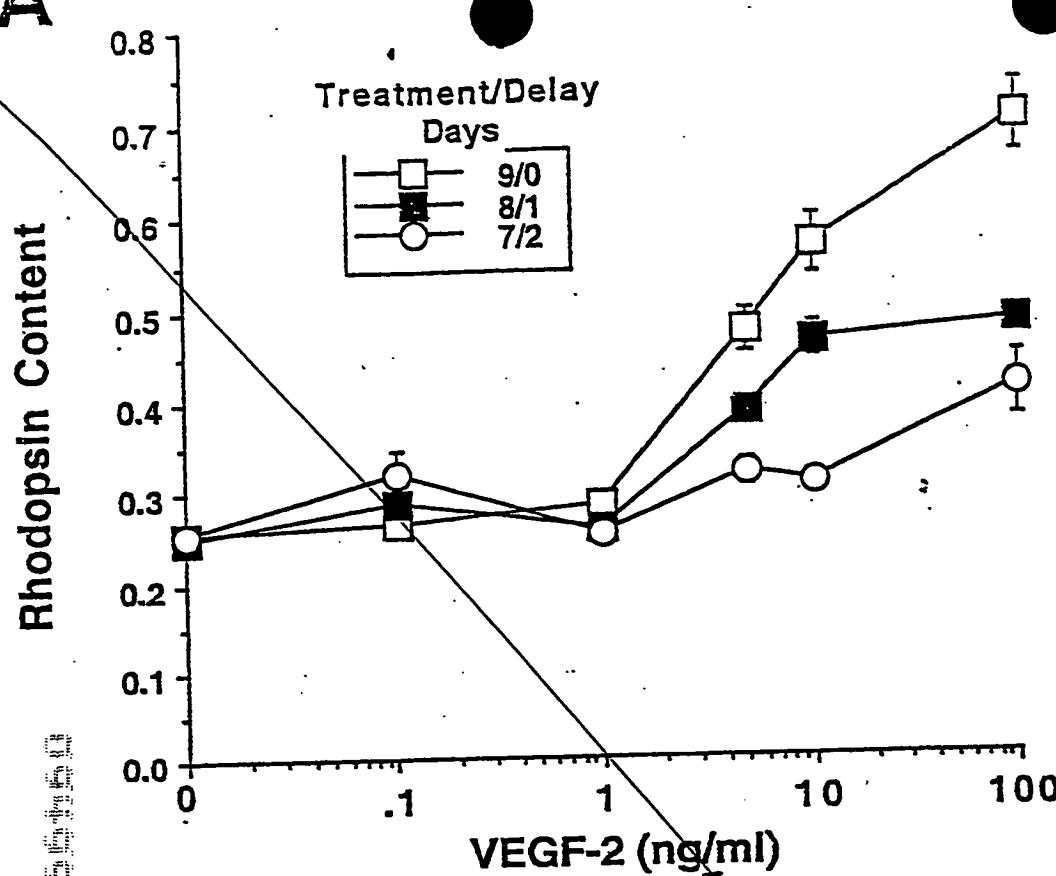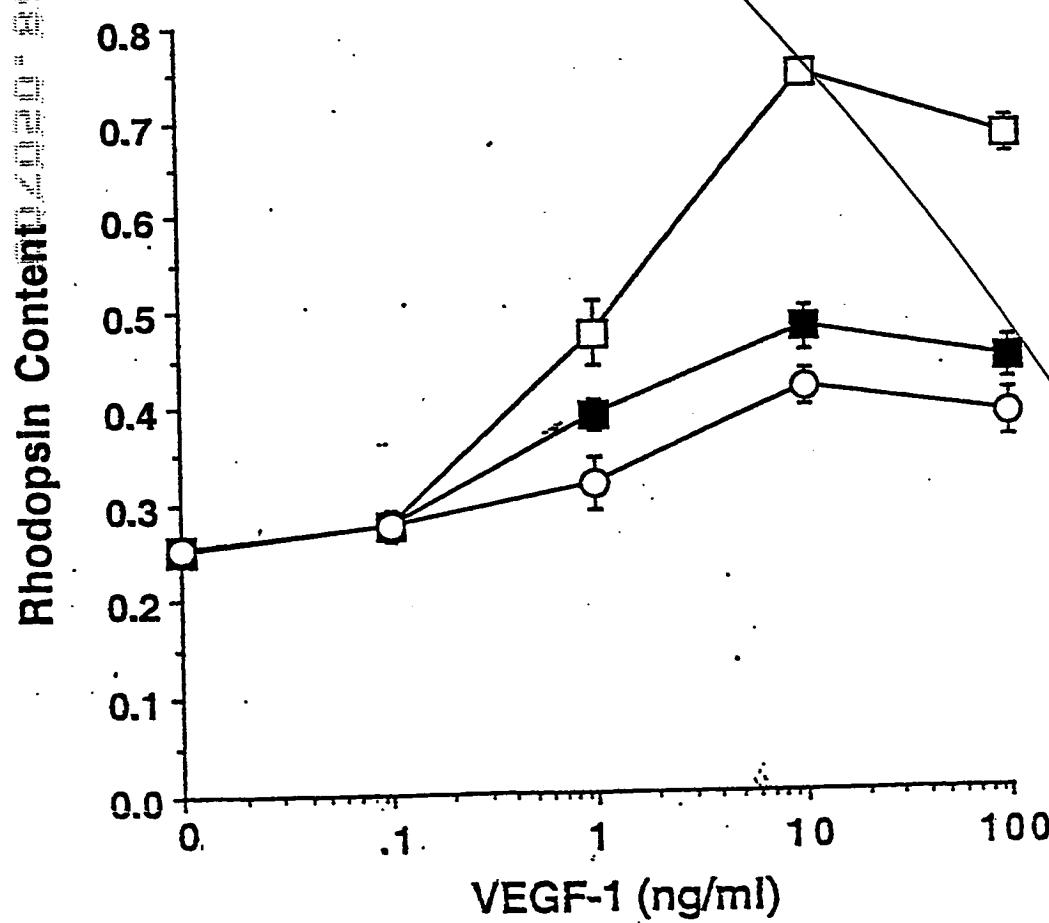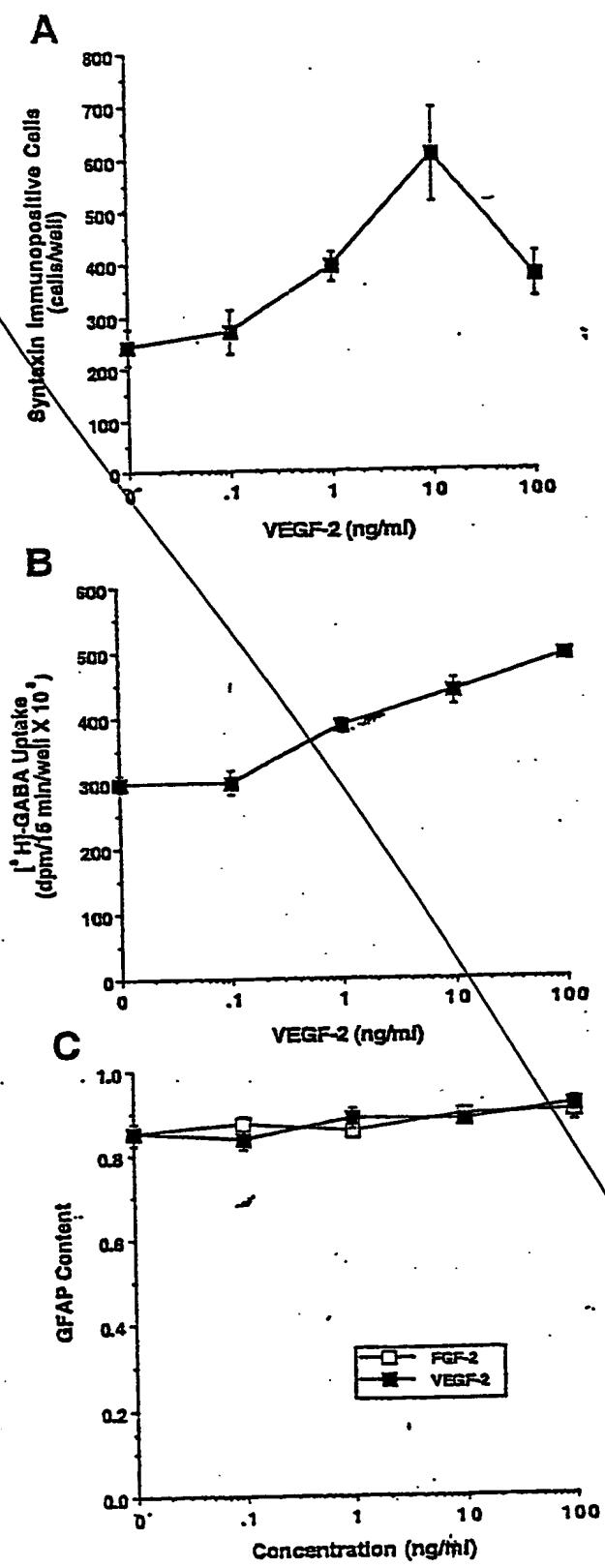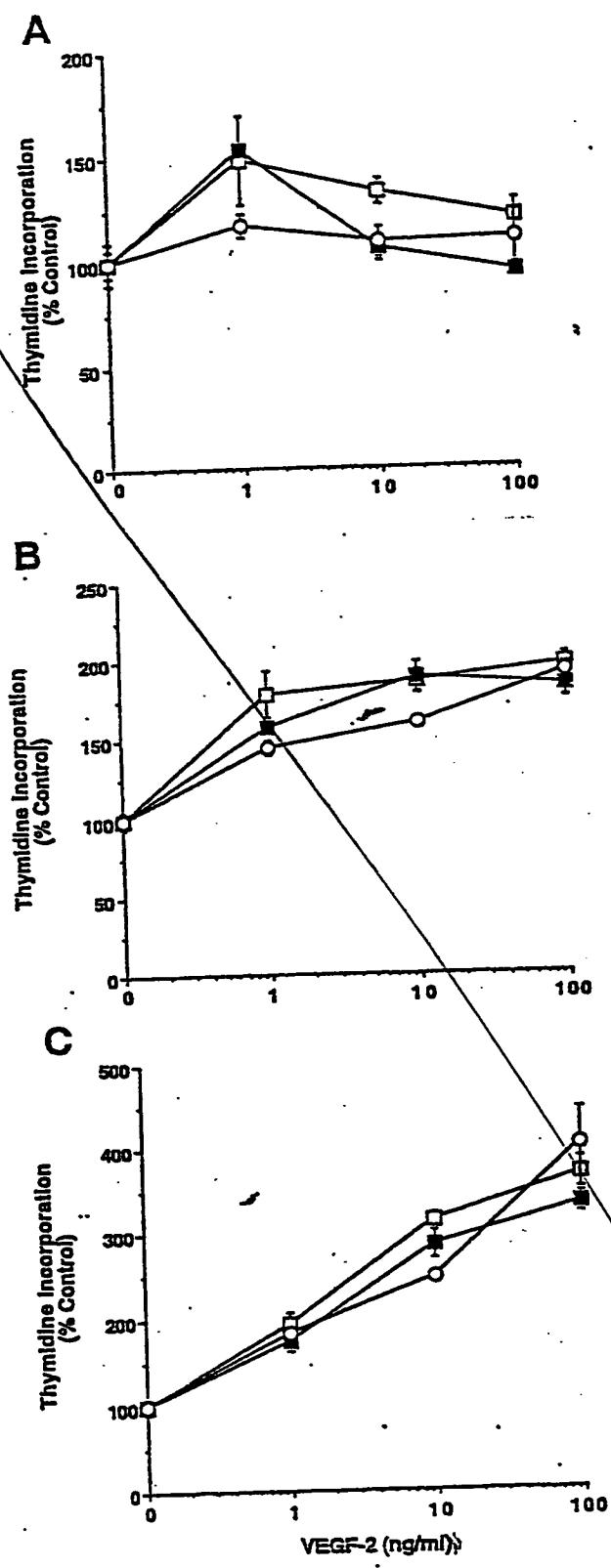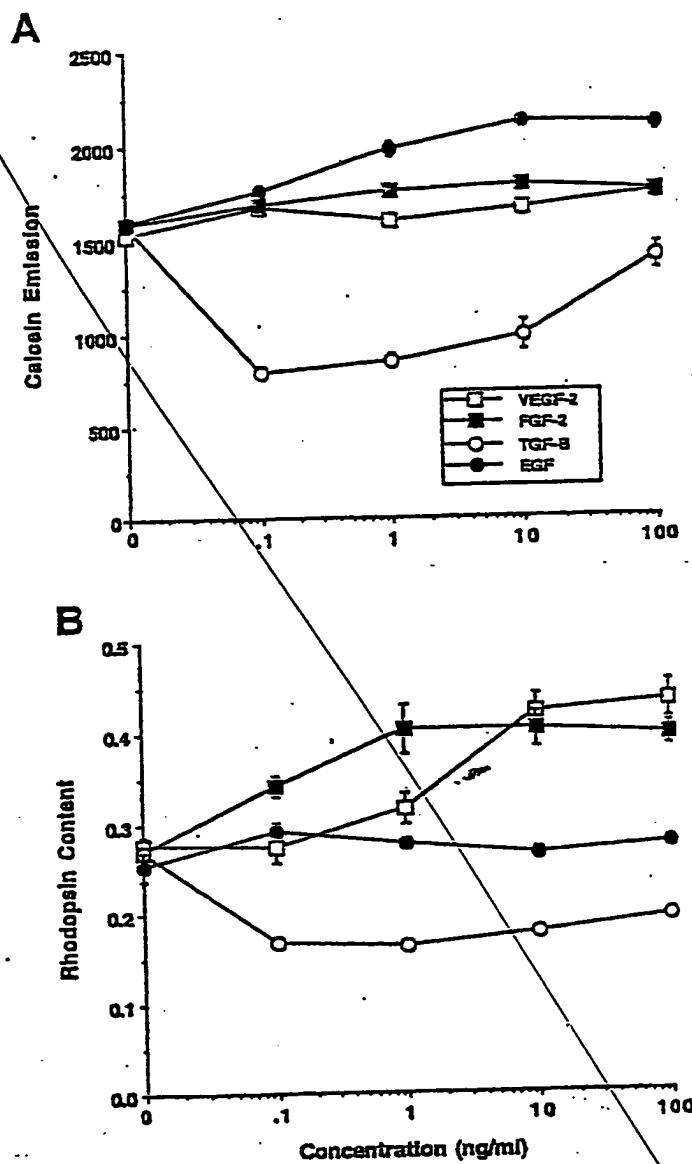
FIG. 22
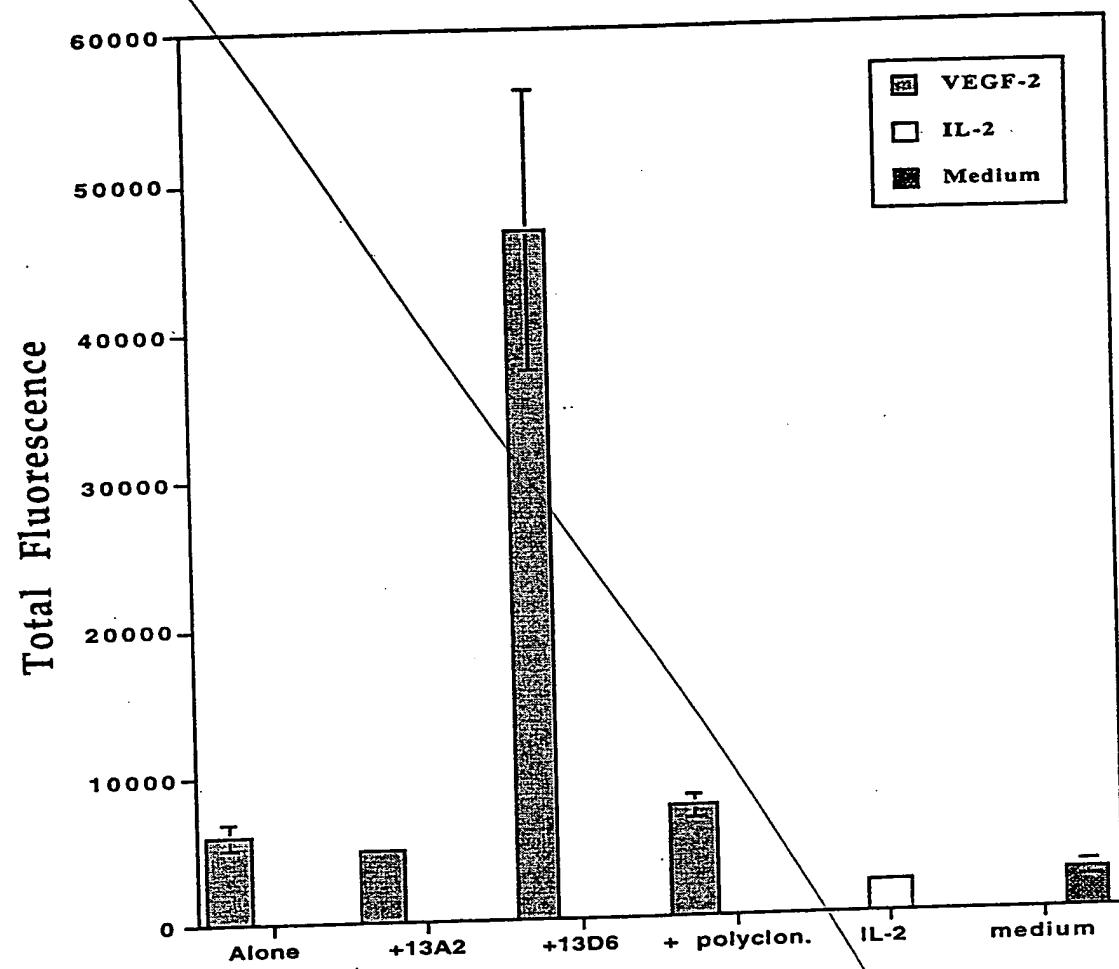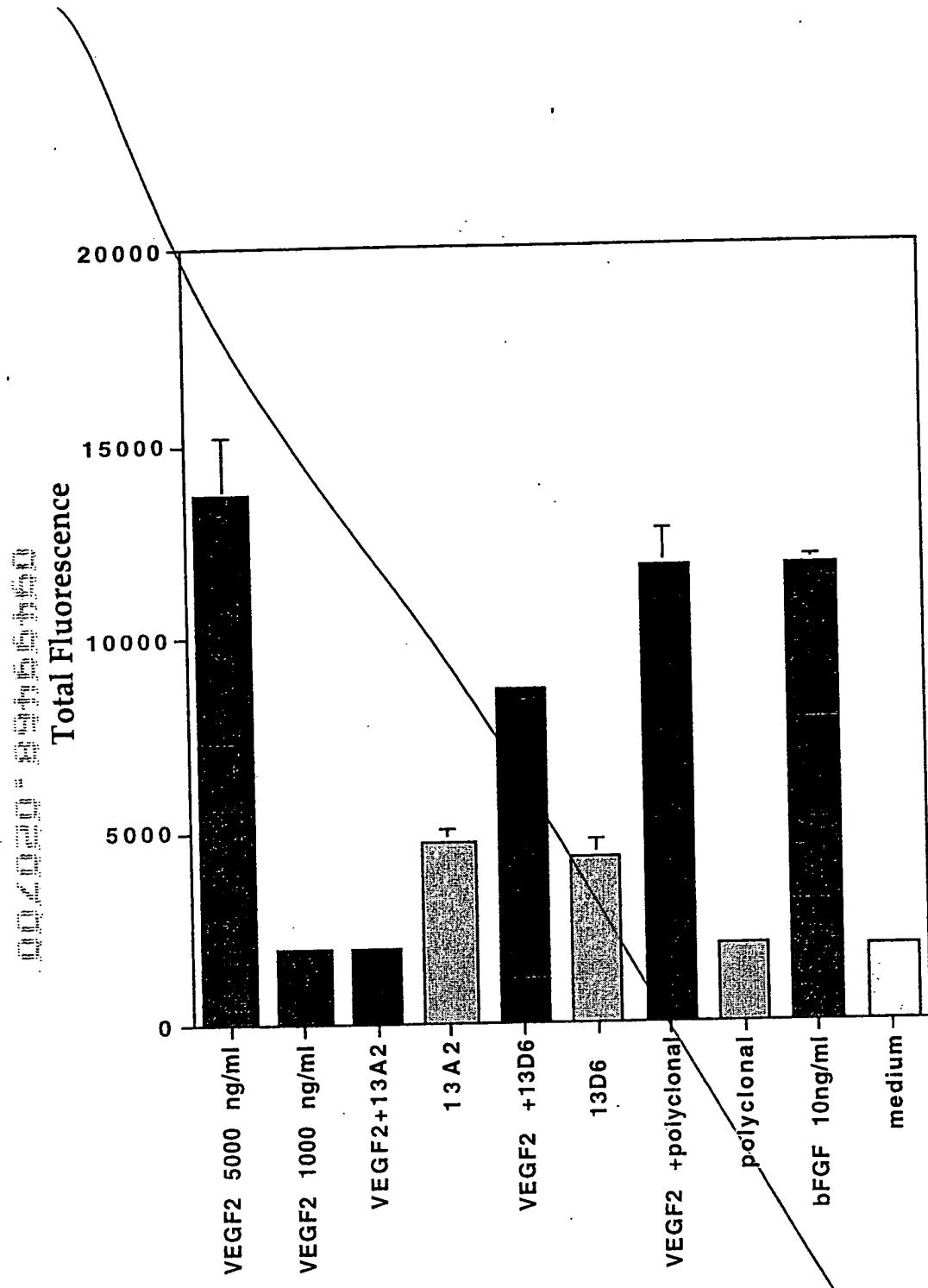
FIG.23

Epitope map for murine anti VEGF-2 MAB

N

32   103   419

19A3
13E6
13D6

C-1
12E2
15C2
13A2

C-3
11A8

C-2
8G11

FIG. 24
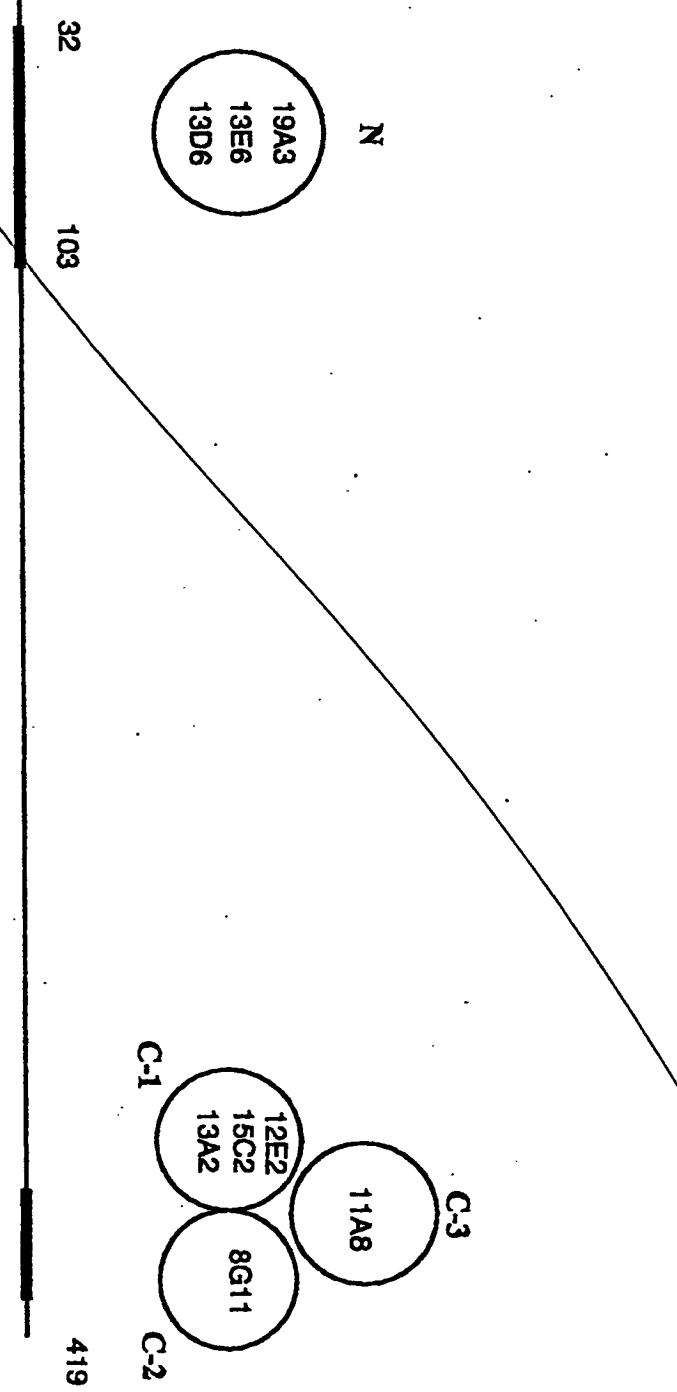
Murine VEGF-2 MAB status

	Isotype	Rel.affinity ng/ml	Specificity	Reactivity Western	ELISA	Purified mg
12E2	γ1	<1	C-1	+		27
13A2	γ1	<1	C-1	n.t	+	27
15C2	γ1	<1	C-1	n.t	+	10
13D6	γ1	<1	N	+	+	25
13E6	γ1	1	N	+	+	38
19A3	γ1	1	N	+	+	54
8G11	γ1	5	C-2	+	+	7
11A8	γ1	<1	C-3	+	+	9

FIG. 25